Zoosyst. Evol. 101 (1) 2025, 245–255 | DOI 10.3897/zse.101.138964

PENSOFT

MUSEUM FÜR NATURKUNDE BERLIN

A new species of *Hemiphyllodactylus* (Squamata, Gekkonidae) from western Yunnan, China

Hongxin Zhou[1,2*], Xiaohan Wang[1*], Liangwei Cui[1], Dongru Zhang[3], Ziqi Shen[2], Xiuyan Li[2], Shuo Liu[2,4], Dingqi Rao[2]

1 *Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Southwest Forestry University, Kunming, Yunnan 650224, China*

2 *Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan 650201, China*

3 *School of Biological Science and Technology, Liupanshui Normal University, Liupanshui, Guizhou 553004, China*

4 *Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan 650223, China*

https://zoobank.org/5C83D016-F105-4D97-8317-8916B792A9A8

Corresponding authors: Dingqi Rao (raodq@mail.kiz.ac.cn); Shuo Liu (liushuo@mail.kiz.ac.cn)

Academic editor: Justin Bernstein ♦ **Received** 10 October 2024 ♦ **Accepted** 29 December 2024 ♦ **Published** 6 February 2025

Abstract

A new species of gekkonid, *Hemiphyllodactylus laowozhenensis* **sp. nov.**, is described based on three specimens from Lushui City, Yunnan, China. The new species can be distinguished from its congeners by a significant genetic divergence of greater than 4.8% in the mitochondrial ND2 gene and a combination of the following characters: maximum SVL of 38.5 mm; 10 or 11 chin scales; enlarged postmentals; 6 circumnasal scales; 2 or 3 internasal scales; 8 or 9 supralabial scales; 8 or 9 infralabial scales; 15 or 16 dorsal scales; 9 ventral scales; a manual lamellar formula of 3-4-4-4 and a pedal lamellar formula of 3(4)-4-4-4; 26–28 precloacal and femoral pore-bearing scales contiguous in males; 1–3 cloacal spur on each side; a dark postorbital stripe extending to at least base of neck; dorsolateral light–colored spots on trunk present; dark ventrolateral stripe on trunk present; dark dorsal transverse blotches present; and a dark and brown postsacral mark bearing anteriorly projecting arms.

Key Words

Hemiphyllodactylus laowozhenensis sp. nov., integrative taxonomy, Lushui City, molecular phylogeny, slender gecko

Introduction

The genus *Hemiphyllodactylus* currently comprises a total of 59 species (Uetz et al. 2024), primarily distributed in South Asia, Southeast Asia, and the Indo-Pacific islands (Zug 2010; Grismer et al. 2013, 2018; Agarwal et al. 2019; Eliades et al. 2019; Agung et al. 2021, 2022; Luu et al. 2023, 2024). It was previously considered a "low-diversity group" (Zug, 2010). However, an integrative taxonomic study by Grismer et al. (2013) revealed that the diversity of *Hemiphyllodactylus* species is much greater than previously thought. Subsequently, the number of *Hemiphyllodactylus* species entered a period of rapid increase (Uetz et al. 2024).

Currently, the majority of newly discovered species of *Hemiphyllodactylus* from Southeast Asia, while the number of species published within China is significantly lower (Uetz et al. 2024). Considering the similar climates between southern China and Southeast Asia, it is plausible that a similar pattern may exist in China (Grismer et al. 2018). Therefore, a large-scale survey is needed in southern China. Yunnan Province, as the most diverse

* These authors contributed equally to this work.

Copyright *Zhou, H. et al.* This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

province for *Hemiphyllodactylus* species in China (8/15), may still harbor numerous cryptic species (Agung et al. 2022; Zhou et al. 2024a, b).

During a recent field survey in Laowo Town, Lushui City, Nujiang Prefecture, Yunnan Province, we collected three specimens of *Hemiphyllodactylus*. The phylogenetic topology resulting from both Maximum Likelihood (ML) and Bayesian Inference (BI) analyses based on ND2 sequences indicates that we have reassigned the collected specimens to a new lineage within Clade 3 of Agung et al. (2022), with *Hemiphyllodactylus longlingensis* as their sister group. Additionally, they exhibit significant morphological differences from other known species. Therefore, we hereby describe them as a new species.

Materials and methods

Specimens and morphology

Three specimens were collected from Laowo Town (Fig. 1), Lushui City, Yunnan Province, China on August 2024. We took samples of liver tissue from each individual specimen and preserved them in 95% ethanol for genetic analysis. The specimens were then stored in 80% ethanol for morphological measurements. All specimens were deposited in Kunming Institute of Zoology (KIZ), Chinese Academy of Sciences (CAS).

The raw lengths of mensural data and meristic characters were taken with a digital calipers to the nearest 0.01 mm under a dissecting microscope (Jiangnan XTB–01) following Zug (2010), Grismer et al. (2013), and Agung et al. (2021, 2022): snout–vent length (**SVL**), taken from the tip of the snout to the vent; tail length (**TL**), taken from the vent to the tip of the tail; trunk length (**TrunkL**), taken from the posterior margin of the forelimb at its insertion point on the body to the anterior margin of the hind limb at its insertion point on the body; head length (**HL**), measured from the posterior margin of the retroarticular process of the lower jaw to the tip of the snout; head width (**HW**), measured at the angle of the jaws; eye diameter (**ED**), the greatest horizontal diameter of the eyeball; snout–eye length (**SnEye**), measured from anterior-most margin of the eyeball to the tip of snout; nares–eye length (**NarEye**), measured from the anterior margin of the eyeball to the posterior margin of the ex-

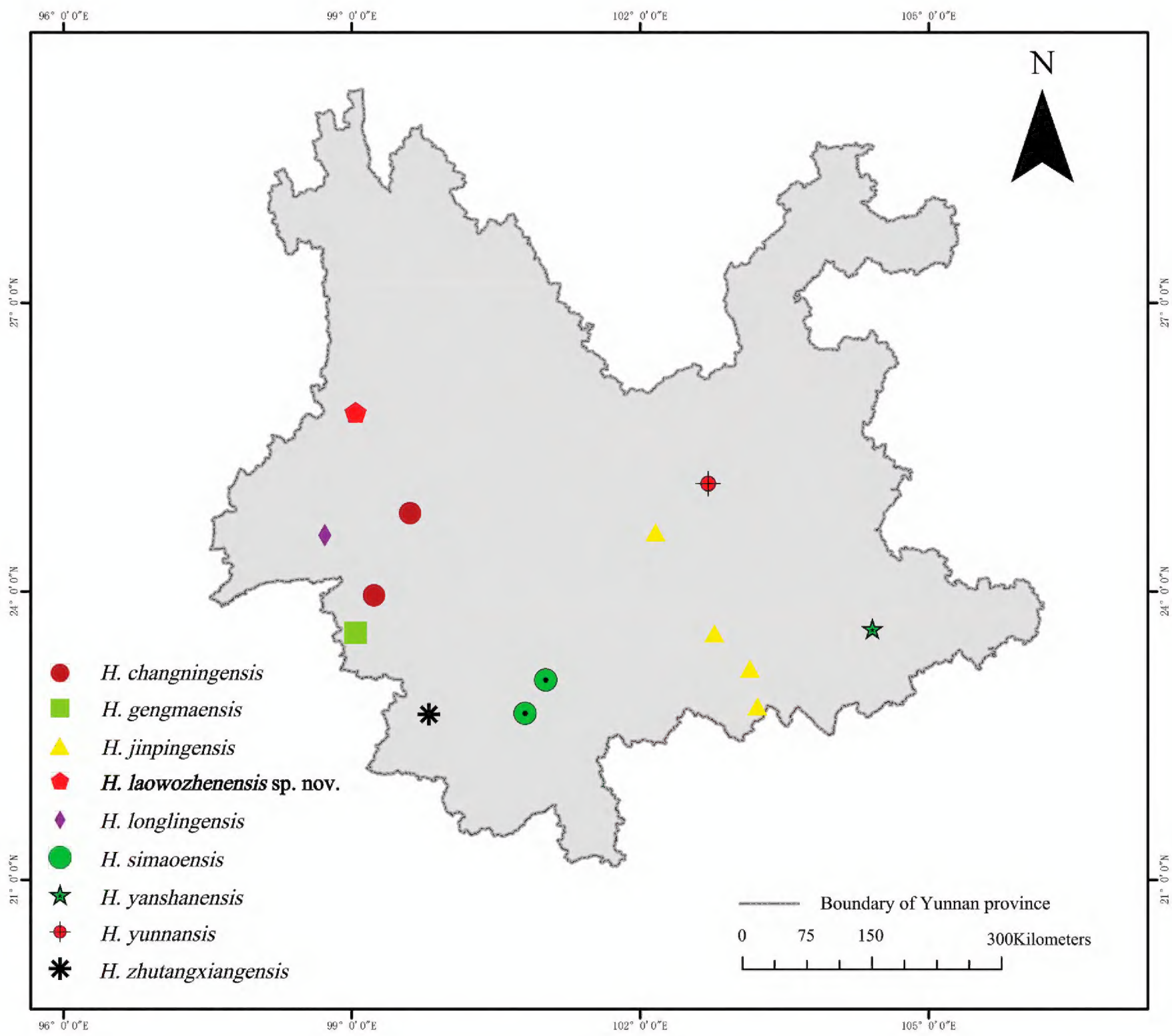

Figure 1. Distribution map of the genus *Hemiphyllodactylus* in Yunnan Province, China.

ternal nares; and snout width (**SnW**), measured between the external nares; chin scales (**Chin**); circumnasal scales (**CN**); internasal scales (**IS**); supralabial (**SL**); infralabial (**IL**); ventral scales (**VS**); dorsal scales (**DS**); subdigital lamellae wider than long on first finger (**SL1F**) and toe (**SL1T**); subdigital lamellae formula determined as number of U-shaped digital pads on digits II–V of hands and feet; number of femoroprecloacal pores; and number of cloacal spurs (**CloacS**) on each side of hemipenial swelling; We also noted coloration and pattern on the dorsum: presence or absence of dark postorbital stripe; presence or absence of dorsolateral light-colored spots on trunk; presence or absence of dark dorsolateral and ventrolateral stripe on trunk; presence or absence of dark dorsal transverse blotches; presence or absence of dark reticulate pattern on dorsum; presence or absence of postsacral marking anteriorly projecting arms.

For the statistical analysis of morphological characteristics, we conducted a statistical analysis on the morphological characteristics within clade 3 (*H. zhutangxiangensis*, *H. changningensis*, *H. gengmaensis*, *H. jinghongensis* and *H. laowozhenensis* sp. nov.). due to the lack of detailed traits of *H. longlingensis* and the availability of only one specimen for *H. zalonicus*, both *H. longlingensis* and *H. zalonicus* were excluded from the statistical analysis. First, we utilized the GroupStruct package in R to adjust the measurement characteristics following Agung et al. (2021, 2022), Luu et al. (2023, 2024), Zhou et al. (2024b); then, we employed Principal Component Analysis (PCA) based on the corrected measurement values and meristic features in the ADEGENET package in R (R Core Team 2021); Finally, we utilized ggplot 2 to visualize the results.

Phylogenetic sampling and analyses

25 sequences of genus *Hemiphyllodactylus* were obtained from GenBank for phylogenetic analyses. GenBank accession numbers of all sequences are shown in Table 1.

Genomic DNA was extracted from liver tissue samples, using Trelief Hi-Pure Animal Genomic DNA Kit from Beijing Tsingke Biotechnology Co., Ltd. We amplified and sequenced the complete mitochondrial NADH dehydrogenase subunit 2 gene (ND2) of three specimens, totaling 1,038 bp using the primers L4437b and H5934 (Macey et al. 1997). The protocol for polymerase chain reaction (PCR) amplifications followed Agung et al. (2021).

DNA sequences were aligned in MEGA 11 (Tamura et al. 2021) by the Clustal W algorithm with default parameters (Thompson et al. 1994). The dataset was tested

Table 1. List of specimens used for phylogenetic analyses in this study.

Species	GenBank no.	Locality	Voucher information
H. harterti	KF219760	Bukit Larut, Malaysia	LSUHC 10383
H. harterti	KF219761	Bukit Larut, Malaysia	LSUHC 10384
H. zhutangxiangensis	MW962150	Zhutangxiang town, Lancang Lahu, Yunnan, China	KIZ061163
H. zhutangxiangensis	MW962151	Zhutangxiang town, Lancang Lahu, Yunnan, China	KIZ061164
H. zhutangxiangensis	MW962152	Zhutangxiang town, Lancang Lahu, Yunnan, China	KIZ061165
H. zhutangxiangensis	MW962153	Zhutangxiang town, Lancang Lahu, Yunnan, China	KIZ061166
H. zhutangxiangensis	MW962154	Zhutangxiang town, Lancang Lahu, Yunnan, China	KIZ061167
H. longlingensis	FJ971045	Longyang District, Baoshan, Yunnan, China	isolate N30
H. longlingensis	FJ971046	Longyang District, Baoshan, Yunnan, China	NJNUh00104
H. longlingensis	FJ971047	Longyang District, Baoshan, Yunnan, China	isolate N32
H. longlingensis	FJ971048	Longyang District, Baoshan, Yunnan, China	isolate N33
H. zalonicus	MW039150	Zalon Taung National Forest, Ban Mauk, Sagaing, Myanmar	ZMMU R 16635
H. changningensis	ON676073	Yongde County, Yunnan, China	KIZ 061990
H. changningensis	ON676074	Yongde County, Yunnan, China	KIZ 061991
H. changningensis	ON676075	Yongde County, Yunnan, China	KIZ 061992
H. changningensis	ON676076	Yongde County, Yunnan, China	KIZ 061993
H. changningensis	ON676077	Yongde County, Yunnan, China	KIZ 061994
H. changningensis	ON676078	Yongde County, Yunnan, China	KIZ 061995
H. changningensis	ON676079	Yongde County, Yunnan, China	KIZ 061996
H. changningensis	ON676080	Yongde County, Yunnan, China	KIZ 061997
H. gengmaensis	PP540023	Gengma Dai and Wa Autonomous County, Yunnan, China	2014002297
H. gengmaensis	PP540024	Gengma Dai and Wa Autonomous County, Yunnan, China	2014002298
H. gengmaensis	PP540022	Gengma Dai and Wa Autonomous County, Yunnan, China	2014002299
H. gengmaensis	PP540021	Gengma Dai and Wa Autonomous County, Yunnan, China	2014002300
H. gengmaensis	PP540025	Gengma Dai and Wa Autonomous County, Yunnan, China	2014002302
H. laowozhenensis sp. nov.	PQ819178	Laowo town, Lushui City, Yunnan, China	LW2024R004
H. laowozhenensis sp. nov.	PQ819179	Laowo town, Lushui City, Yunnan, China	LW2024R005
H. laowozhenensis sp. nov.	PQ819180	Laowo town, Lushui City, Yunnan, China	LW2024R006

for the best-fit substitution model of ML and BI respectively in ModelFinder v. 2.2.0 (Kalyaanamoorthy et al. 2017) with Akaike and Bayesian Information Criteria. A maximum-likelihood (ML) analysis was conducted using TN+F+G4 as the best-fit substitution model. We applied 1,000 bootstrap pseudoreplicates with the ultrafast bootstrap approximation algorithm (UFBoot), where nodes having values of 95 and above were considered highly supported (Minh et al. 2013). A Bayesian-inference (BI) analysis was conducted using GTR+F+G4 model following the methods by Agung et al. (2021). We ran two independent Markov Chain Monte Carlo (MCMC) analyses with four chains in each analysis (three hot and one cold). The MCMC analyses were implemented with 10 million generations, sampled every 5000 generations with the first 10% sampled discarded as burn-in. Nodes with Bayesian posterior probabilities (BPP) of 0.95 and above were considered highly supported (Huelsenbeck et al. 2001; Wilcox et al. 2002). Uncorrected pairwise divergences were calculated using MEGA 11 (Tamura et al. 2021).

Species delineation

Our species definition and species delimitation methods are based on Agung et al. (2022): first, new lineages not clustered within the named species lineages in phylogenetic topology were marked as potential new species; second, uncorrected pairwise genetic distances among the new lineages with either known species or other putative species lineages were measured, with a 3.0% difference in mtDNA ND2 considered minimal to define a potential new species; third, those lineages showing >3.0% genetic difference from their nearest relatives were examined for morphological distinctiveness from closely related species. If this third criterion was also met, the lineage was considered a confirmed new species.

Results

Our phylogenetic topology is consistent with previously published studies (Grismer et al. 2013; Grismer et al. 2020; Agung et al. 2021, 2022; Yushchenko et al. 2023). The ML and BI analyses (Fig. 2) recovered the Laowo town populations to be nested within clade 3 of Agung et al. (2022). The phylogenetic analyses recovered a strongly-supported monophyletic lineage containing all *Hemiphyllodactylus* samples used in this study (ML 100/BI 1.00). Uncorrected genetic P-distances among and within the ND2 gene of the newly recovered OTUs (within clades 3) are presented in Table 2. The mean percentage of uncorrected pairwise distance between the Laowo Town specimens and its sister species *H. longlingensis* is 4.8% (Table 2). The clustering of species in the PCA of Clade 3 showed the first two principal components (PC1 and PC2) recovered 65.45% of the variation in the normalized morphometric and meristic dataset (Fig. 3, Suppl. material 1). PC1 represented 50.65% of the dataset variability, with the heaviest loadings for DS, VS, Chin and CN, while PC2 represented 14.80% of the dataset variability, with the heaviest loadings for HW, Chin, DS and CN. The PCA recovered *Hemiphyllodactylus laowozhenensis* sp. nov. to be widely separated from other species.

Based on the molecular and morphological evidence, we hereby describe these specimens from Laowo Town as a new species, *Hemiphyllodactylus laowozhenensis* sp. nov.

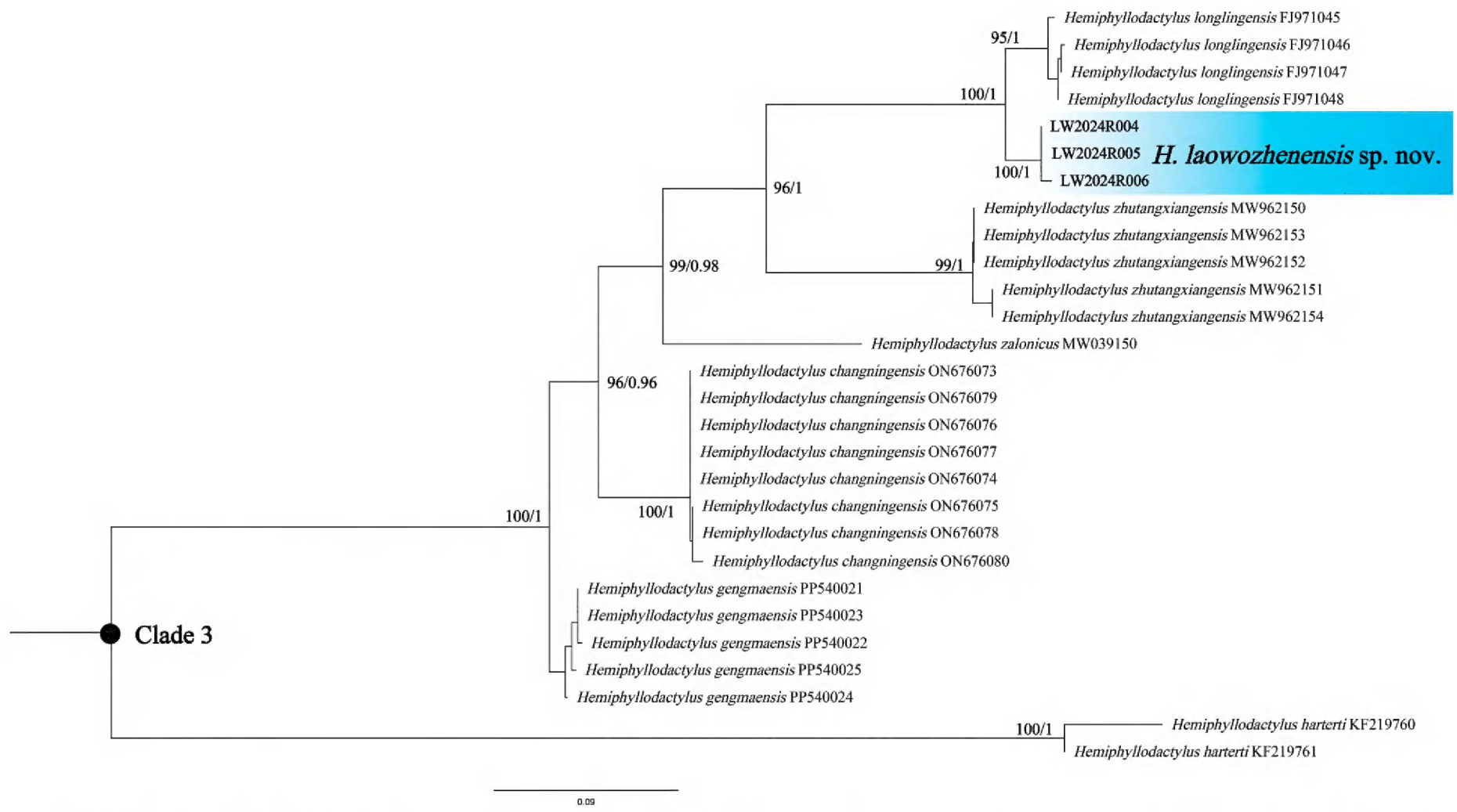

Figure 2. Maximum-likelihood consensus tree mitochondrial ND2 gene. Numbers by the nodes indicate ML bootstrap support values and posterior probability values of the BI.

Table 2. The mean percentage of the uncorrected p–distance among the *Hemiphyllodactylus* species studied based on mitochondrial ND2 gene fragments.

Species name (no.)	1	2	3	4	5	6
1. *H. gengmaensis* (5)						
2. *H. longlingensis* (4)	24.4					
3. *H. zalonicus* (2)	17.2	26.9				
4. *H. zhutangxiangensis* (5)	20.3	22.5	24.2			
5. *H. changningensis* (8)	9.6	25.5	19.0	22.0		
6. *H. laowozhenensis* (3)	**24.0**	**4.8**	**27.5**	**21.8**	**25.5**	

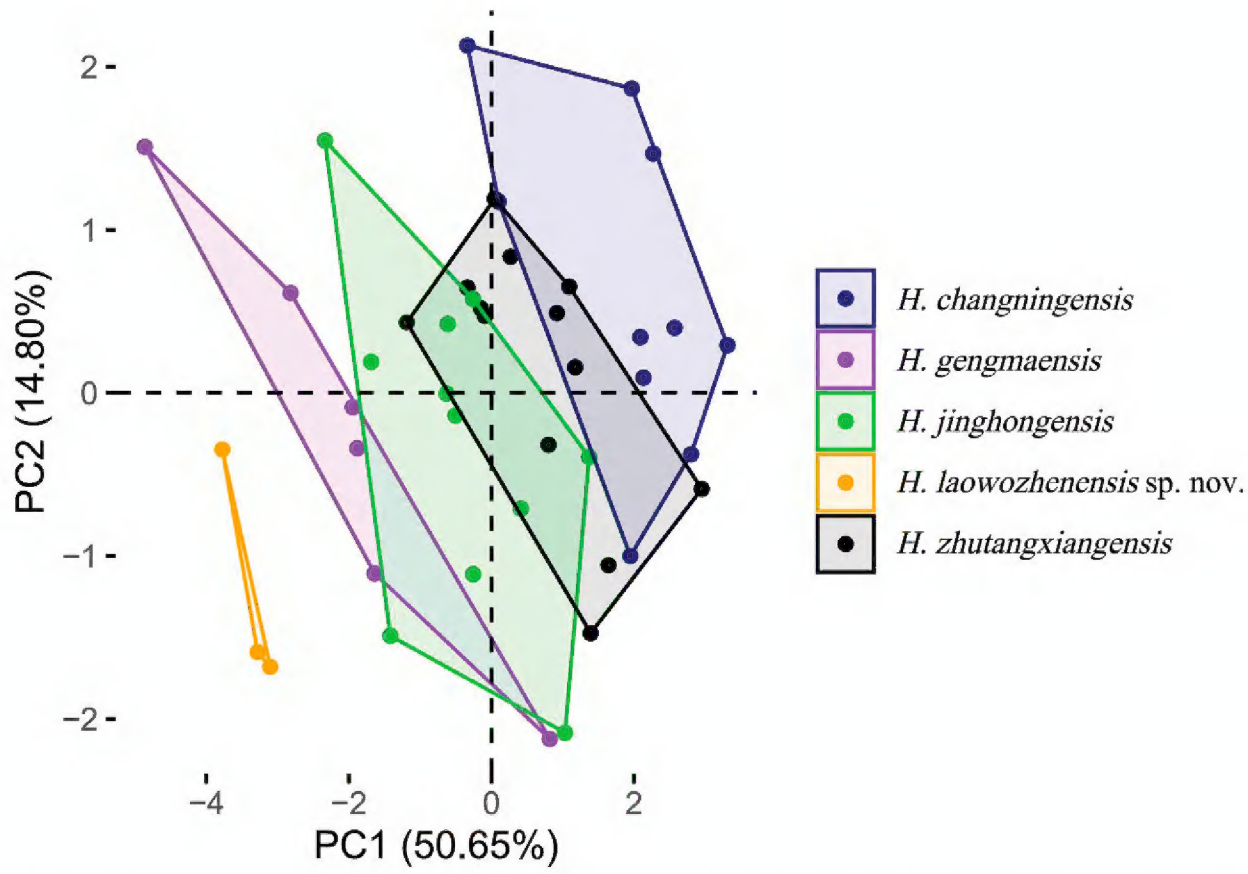

Figure 3. PCA of *Hemiphyllodactylus* species between new species with their related species showing their morphospatial relationships along the first two principal components based on their morphological traits (Suppl. material 2).

Taxonomic account

***Hemiphyllodactylus laowozhenensis* sp. nov.**

https://zoobank.org/DE9C8C1E-CAF1-4280-BE45-359157B79B39

Fig. 4

Type material. ***Holotype.*** • LW2024R006, adult male, collected by Hongxin Zhou, Xiuyan Li, Jiazhong Wang on August 2024 from Laowo Town, Lushui City, Yunnan, China (25.865°N, 99.038°E, at an elevation of 1511 m).

Paratypes. • LW2024R004, LW2024R005, adult males, collected at the same locality as the holotype on August 2024.

Diagnosis. *Hemiphyllodactylus laowozhenensis* sp. nov. can be distinguished from its congeners by the combination of the following characters: maximum SVL of 38.5 mm; 10 or 11 chin scales; enlarged postmentals; 6 circumnasal scales; 2 or 3 internasal scales; 8 or 9 supralabial scales; 8 or 9 infralabial scales; 15 or 16 dorsal scales; 9 ventral scales; a manual lamellar formula of 3-4-4-4 and a pedal lamellar formula of 3(4)-4-4-4; 26–28 precloacal and femoral pore-bearing scales contiguous in males; 1–3 cloacal spur on each side; a dark postorbital stripe extending to at least base of neck; dorsolateral light–colored spots on trunk present; dark ventrolateral stripe on trunk present; dark dorsal transverse blotches present; and a dark and brown postsacral mark bearing anteriorly projecting arms.

Description of holotype. Adult male, one longitudinal incision on ventral surface used for liver tissue sampling, small–sized (SVL 38.30 mm), and somewhat flattened in body shape; head triangular, elongated (HL/SVL = 0.25); dorsum of head covered in granular scales, which are relatively small; six circumnasal scales, with the lower two being the rostral and the largest upper labial, while the other three are circular; two internasal scales; circular mental scale; ten chin scales touching the internal edges of the infralabials, extending from the juncture of the 2nd and 3rd infralabial scales on the left of the mental scale to the same juncture on the right (Chin); scales in the gular region are rounded, non–overlapping, becoming larger and more ovoid on the venter; snout short and narrow (SnW = 1.57 mm; SnW/HL = 0.16); small eyes (ED = 2.48 mm; ED/HL = 0.25); robust body shape (TrunkL/SVL=0.54); granular scales on the dorsum, with 16 scales within one eye diameter; ventral scales are flattened, with 9 scales within one eye diameter; granular scales on the limbs; Finger I is vestigial,

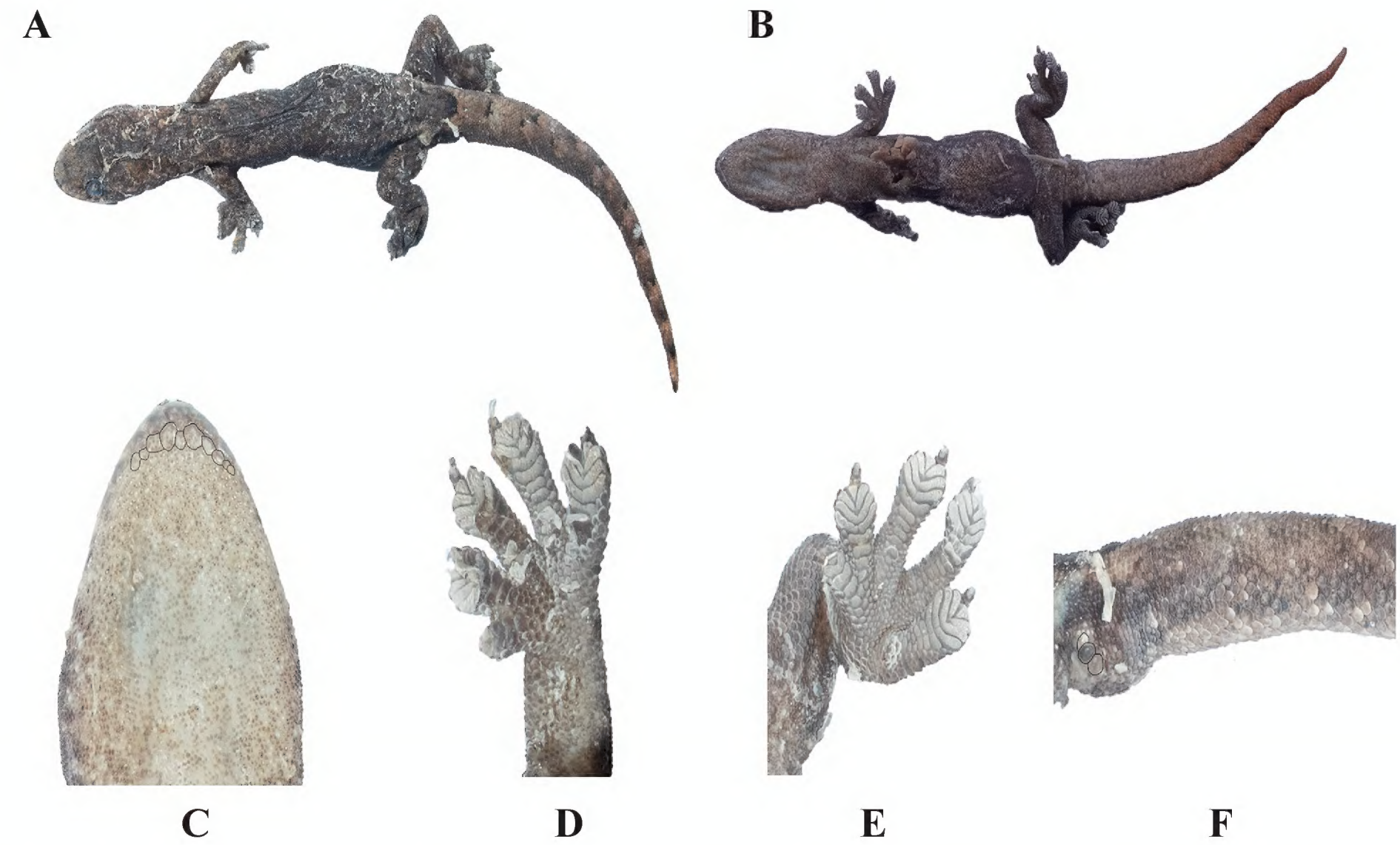

Figure 4. *Hemiphyllodactylus laowozhenensis* sp. nov. **A.** Holotype, LW2024R006, dorsal view in alcohol; **B.** Holotype, LW2024R006, ventral view in alcohol; **C.** The ventral view of the head; black lines indicate chin scales; **D, E.** In view of lamellae formula counting on fingers and feet I to V; **F.** Lateral view of basal tail.

clawless, and with rectangular subdigital lamellae, while Fingers II–V are well–developed; the proximal subdigital lamellae are undivided and rectangular, while the distal subdigital lamellae are divided, angular, U–shaped, except for the terminal lamellae, which are rounded and undivided; subdigital lamellae count 3-4-4-4 (hand) and 4-4-4-4 (foot); femoral pores and precloacal pores continuous, with a total count 28; Tail long (TL/SVL = 0.90), with dorsal scales larger than those on the body and head, and smaller than the subcaudals; subcaudals are large and flat.

Coloration in ethanol. The dorsal surface of head and body is dark-gray; dark stripes extend from the posterior corner of the eye socket to the neck; the back is covered with dark and light-colored dorsal transverse blotches; the dorsal surfaces of the limbs are dark; the dorsal surface of tail is brown-gray, with several dark-brown transverse stripes and its ventral surface is orange-red; the ventral surfaces of the head are gray with dark spots; the ventral surfaces of the body are dark.

Variation. The primary variations observed in this species pertain to scale counts and morphometric data, which are comprehensively documented in Table 3.

Distribution. This species is currently known to be distributed at the type locality Laowo Town, Lushui City of Yunnan Province in China (Fig. 1).

Natural history. *Hemiphyllodactylus laowozhenensis* sp. nov. was discovered on the walls of houses situated alongside the streets of Laowo Town, where its population is scant. It coexists in the same region with the *Hemidactylus aquilonius*.

Etymology. The scientific name "*laowozhenensis*" is derived from its type locality Laowo Town, Lushui City in Yunnan province. We suggest Laowo Town Slender Gecko in English and "老窝镇半叶趾虎 (Lǎo Wō Zhèn Bàn Yè Zhǐ Hǔ)" in Chinese.

Comparisons. We compared the morphology of *Hemiphyllodactylus laowozhenensis* against its closely related species, specifically species from clade 3, as inferred from the phylogeny we constructed (Table 4).

H. laowozhenensis sp. nov. differences from *H. gengmaensis* by shorter head (HL = 9.71–9.96 versus 10.80–11.24; HL/SVL = 0.25–0.26 versus 0.26–0.31); shorter SnEye distance (SnEye = 3.43–3.64 versus 3.88–4.52; SnEye/HL = 0.35–0.37 versus 0.36–0.41); thinner SnW distance (SnW = 1.60–1.57 versus 1.60–2.72); smaller eyes (ED/HL=0.22–0.24 versus 0.24–0.25); more chin scales (10 or 11 versus 8 or 9); few supralabial scales (SL = 8 or 9 versus 9–11); few lamelar fomnlae hands and foot II-V (hands = 3-4-4-4 versus 5-5(6)-5-4; foot = 3(4)-4-4-4 versus 5-5-6-5); few SL1F (SL1F = 4 versus 5); few SL1T (SL1T = 4 versus 6); more femoroprecloacal pores (26–28 versus 10–25); dorsolateral light–colored spots on trunk present (versus absent); dark ventrolateral stripe on trunk present (versus absent); dark reticulate pattern on dorsum absent (versus Yes or Indistinct).

H. laowozhenensis sp. nov. differences from *H. longlingensis* by shorter head (HL/SVL = 0.25–0.26

Table 3. Mensural (in mm), meristic, color pattern, and proportions of the type series of *Hemiphyllodactylus laowozhenensis* sp. nov.

Character	Holotype	Paratype	Paratype
	LW2024R006	LW2024R004	LW2024R005
Sex	Male	male	male
SVL	38.30	36.74	38.50
TL	34.58	31.90	32.30
TrunkL	20.5	18.76	19.84
HL	9.73	9.71	9.96
HW	6.66	7.41	7.22
ED	2.48	2.42	2.4
SnEye	3.64	3.43	3.56
NarEye	2.88	2.94	2.92
SnW	1.57	1.6	1.58
TrunkL/SVL	0.54	0.51	0.52
HL/SVL	0.25	0.26	0.26
HW/SVL	0.17	0.20	0.19
HW/HL	0.68	0.76	0.72
SnEye/HL	0.37	0.35	0.36
NarEye/HL	0.30	0.30	0.29
ED/HL	0.25	0.25	0.24
SnW/HL	0.16	0.16	0.16
ED/NarEye	0.86	0.82	0.82
Snw/HW	0.24	0.22	0.22
Chin	10	11	11
CN	6	6	6
IS	2	3	2
SL (left/right)	8/8	8/8	8/9
IL (left/right)	8/8	8/8	9/9
VS	9	9	9
DS	16	15	15
Lamelar formulae hands II–V (left)	3-4-4-4	3-4-4-4	3-4-4-4
Lamelar formulae hands II–V (right)	3-4-4-4	3-4-4-4	3-4-4-4
Lamelar formulae foot II–V (left)	4-4-4-4	3-4-4-4	3-4-4-4
Lamelar formulae foot II–V (right)	4-4-4-4	3-4-4-4	3-4-4-4
SL1F	4/4	4/4	4/4
SL1T	4/4	4/4	4/4
Precloacal and femoral pore series separate (1) or continuous (0)	0	0	0
Total femoroprecloacal pores	28	26	28
CloacS on each side	3/2	1/1	1/1
Subcaudals enlarged, plate-like	No	No	No
Dark postorbital stripe	Yes	Yes	Yes
Dorsolateral light-colored spots on trunk	Yes	Yes	Yes
Dark dorsolateral stripe on trunk	No	No	No
Dark ventrolateral stripe on trunk	Yes	Yes	Yes
Dark dorsal transverse blotches	Yes	Yes	Yes
Dark reticulate pattern on dorsum	No	No	No
Postsacral marking anteriorly projecting arms	Yes	Yes	Yes

versus 0.22–0.24); longer SnEye distance (SnEye/HL = 0.35–0.37 versus 0.42–0.45); smaller eyes (ED/HL=0.22–0.24 versus 0.15–0.18); more chin scales (10 or 11 versus 7–9); more circumnasal scales (CN = 6 versus 5); more ventral scales contained with one eye diameter (VS = 8 or 9 versus 6–7); more dorsal scales contained with one eye diameter (DS = 15 or 16 versus 10–14); dorsolateral light–colored spots on trunk present (versus absent); dark ventrolateral stripe on trunk present (versus absent).

H. laowozhenensis sp. nov. differences from *H. zalonicus* by longer head (HL = 9.71–9.96 versus 8.4–8.5; HL/SVL = 0.25–0.26 versus 0.22–0.23); wider head (HW = 6.66–7.41 versus 5.7–5.8; HW/SVL = 0.17–20 versus 0.15; HW/HL = 0.68–0.76 versus 0.68); longer NarEye

Table 4. Diagnostic characters separating *Hemiphyllodactylus laowozhenensis* sp. nov. from other nominal taxa of *Hemiphyllodactylus* within clade 3 of Agung et al. (2022). (/) = data unavailable. Mensural characters are in mm. Data for *H. zalonicus* and *H. longlingensis* were obtained from Grismer et al. (2020). Data for *H. changningensis* were obtained from Guo et al. (2015). Data for *H. zhutangxiangensis* were obtained from Agung et al. (2021). Data for *H. gengmaensis* were obtained from Zhou et al. (2024a).

Character	*H. gengmaensis*	*H. longlingensis*	*H. zalonicus*	*H. changningensis*	*H. zhutangxiangensis*	*H. laowozhenensis* sp. nov.
Max SVL	43.24	45.7	37.7	43.8	44.42	38.5
n	6		2	10	13	3
TrunkL	17.46–23.22	/	18.1–18.9	17.4–22.5	16.1–23.1	18.76–20.5
HL	10.8–11.24	/	8.4–8.5	8.2–10.1	6.2–7.6	9.71–9.96
HW	6.88–8.2	/	5.7–5.8	6.1–7.5	6.5–8.2	6.66–7.41
ED	2.12–2.62	/	2.0–2.6	1.7–2.3	2.1–2.7	2.40–2.48
SnEye	3.88–4.52	/	3.4–3.5	3.5–4.5	3.4–4.4	3.43–3.64
NarEye	2.72–3.32	/	2.4–2.7	2.8–3.4	2.6–3.2	2.88–2.94
SnW	1.6–2.72	/	1.2	1.1–1.4	1.3–1.6	1.57–1.60
TrunkL/SVL	0.45–0.54	0.47–0.52	0.49–0.50	0.46–0.51	0.48–0.52	0.51–0.54
HL/SVL	0.26–0.31	0.22–0.24	0.22–0.23	0.22–0.25	0.17–0.20	0.25–0.26
HW/SVL	0.19–0.2	0.17–0.19	0.15	0.17–0.18	0.18–0.20	0.17–0.20
HW/HL	0.64–0.74	0.75–0.80	0.68	0.72–0.80	1.03–1.13	0.68–0.76
SnEye/HL	0.36–0.41	0.42–0.45	0.40–0.42	0.41–0.49	0.53–0.60	0.35–0.37
NarEye/HL	0.24–0.30	0.29–0.34	0.28–0.31	0.30–0.37	0.39–0.44	0.29–0.30
ED/HL	0.20–0.24	0.22–0.25	0.23–0.30	0.21–0.25	0.30–0.36	0.24–0.25
SnW/HL	0.15–0.24	0.12–0.14	0.14	0.12–0.16	0.19–0.22	0.16
ED/NarEye	0.73–0.94	0.66–0.82	0.74–1.08	0.61–0.77	0.70–0.91	0.82–0.86
Snw/HW	0.22–0.33	0.15–0.18	0.21	0.16–0.20	0.16–0.21	0.22–0.24
Chin	8–9	7–9	8–10	7–8	7–9	**10 or 11**
CN	6	4–5	5	3–4	5	**6**
IS	2–3	1–3	3–4	2–3	2–4	2 or 3
SL	9–11	9–10	10	8–11	8–11	8 or 9
IL	8–9	8–10	8–9	8–10	8–11	8 or 9
VS	8–10	6–7	9–10	6–8	5–7	8 or 9
DS	11–18	10–14	17–18	11–15	11–15	**15 or 16**
Lamelar formulae hands II–V	5-5(6)-5-4	3-4-4-4(3) 4-4-4(5)-4	3-3-3-3	3-3(4)-3(4)-3	(3-5)-(4-6)-(4 or 5)-(4 or 5)	3-4-4-4
Lamelar formulae foot II–V	5-5-6-5	4-4(5)-4(5)-4	3-4-4-4	3-3-3-3 3-4-4-4	(4 or 5)-(4 or 5)-4-6-(4 or 5)	3(4)-4-4-4
SL1F	5	4-5	3	3–4	4–5	4
SL1T	6	4-6	4	3–4	4–5	4
Precloacal and femoral pore series separate (1) or continuous (0)	0	0	0	0	0	0
Total femoroprecloacal pores	10–25	16–27	16–20	19–22	20–23	**26-28**
CloacS on each side	1 or 2	1 or 2	1	1 or 2	1 or 2	1–3
Subcaudals enlarged, plate-like	No	No	No	No	No	No
Dark postorbital stripe	Yes	Yes	Yes	Yes	Yes	Yes
Dorsolateral light-colored spots on trunk	No	No	No	No	No	Yes
Dark dorsolateral stripe on trunk	No	No	No	No	No	No

Character	*H. gengmaensis*	*H. longlingensis*	*H. zalonicus*	*H. changningensis*	*H. zhutangxiangensis*	*H. laowozhenensis* sp. nov.
Dark ventrolateral stripe on trunk	No	No	No	No	No	Yes
Dark dorsal transverse blotches	Yes	Variable	No	Yes	Yes	Yes
Dark reticulate pattern on dorsum	Yes or Indistinct	Variable	No	Yes	No	No
Postsacral marking anteriorly projecting arms	Indistinct or Fork-like dark-colored	Light-colored	Indistinct or not	No	Fork-like dark-colored	Yes

distance (NarEye = 2.88–2.94 versus 2.4–2.7); wider SnW distance (SnW = 1.57–1.60 versus 1.20; SnW/HL = 0.16 versus 0.14; SnW/HW = 0.22–0.24 versus 0.21); more chin scales (10 or 11 versus 8–10); more circumnasal scales (CN = 6 versus 5); few supralabial scales (SL = 8 or 9 versus 10); few dorsal scales contained with one eye diameter (DS = 15 or 16 versus 17–18); more SL1F (SL1F = 4 versus 3); more femoroprecloacal pores (26–28 versus 16–20); dorsolateral light–colored spots on trunk present (versus absent); dark ventrolateral stripe on trunk present (versus absent); dark dorsal transverse blotches present (absent).

H. laowozhenensis sp. nov. differences from *H. changningensis* by greater eyes (ED = 2.40–2.48 versus 1.7–2.3); wider SnW distance (SnW = 1.57–1.60 versus 1.10–1.40; SnW/HL = 0.16 versus 0.12–0.16); more chin scales (10 or 11 versus 7 or 8); more circumnasal scales (CN = 6 versus 3 or 4); more femoroprecloacal pores (26–28 versus 19–22); dorsolateral light–colored spots on trunk present (versus absent); dark ventrolateral stripe on trunk present (versus absent); dark reticulate pattern on dorsum absent (versus present); postsacral marking anteriorly projecting arms present (versus absent).

H. laowozhenensis sp. nov. differences from *H. zhutangxiangensis* by longer head (HL = 9.71–9.96 versus 6.2–7.6; HL/SVL = 0.25–0.26 versus 0.17–0.20); more chin scales (10 or 11 versus 7–9); more circumnasal scales (CN = 6 versus 5); more ventral scales contained with one eye diameter (VS = 8 or 9 versus 5–7); more dorsal scales contained with one eye diameter (DS = 15 or 16 versus 11–15); more femoroprecloacal pores (26–28 versus 20–23); dorsolateral light–colored spots on trunk present (versus absent); dark ventrolateral stripe on trunk present (versus absent).

Discussion

Our research supports the recognition of the *Hemiphyllodactylus laowozhenensis* sp. nov. as a new species, belonging to clade 3 of Agung et al. (2022). It is sister taxa to *H. longlingensis*, *H. zalonicus*, *H. changningensis*, *H. zhutangxiangensis* and *H. gengmaensis*. Our research team had overlooked species of this genus during our more than 10 years of surveys in the region. The discovery of this new species further emphasizes the importance of repeated surveys in determining true local species diversity and highlights the diversity of *Hemiphyllodactylus* species in Yunnan Province, China.

In Yunnan Province, our decade-long surveys have found that all habitats of *Hemiphyllodactylus* are adjacent to human settlements, which are precisely areas that are not protected. Most *Hemiphyllodactylus* species in Yunnan have narrow distributions, occurring in only one or several limited number of localities. Therefore, the conservation of *Hemiphyllodactylus* species in the future may face significant challenges.

Ethical statement

The Ethics Committee of Kunming Institute of Zoology, Chinese Academy of Sciences, approved the study and provided ethics permission (no. SMKX-20191221-216).

Funding

This work was supported by Science Technology Basic Condition Platform from the Ministry of Science and Technology of the People's Republic of China (grant no. 2005DKA21402), National Natural Science Foundation Project: Investigation and Classificatory and Phylogenetic Studies on the Lizards of Gekkonidae of China (grant no. NSFC–31970404).

Acknowledgements

We thank Jiazhong Wang for assistance in the field. We also thank the editors and reviews for their comments on the manuscript.

References

Agarwal I, Khandekar A, Giri VB, Ramakrishnan U, Karanth KP (2019) The hills are alive with geckos! A radiation of a dozen species on sky islands across peninsular India (Squamata: Gekkonidae, *Hemiphyllodactylus*) with the description of three new species. Organ-

isms Diversity & Evolution 19: 341–361. https://doi.org/10.1007/s13127-019-00392-5

Agung AP, Grismer LL, Grismer JL, Quah ES, Chornelia A, Lu JM, Hughes LC (2021) A new species of *Hemiphyllodactylus* Bleeker (Squamata: Gekkonidae) from Yunnan, China and its phylogenetic relationship to other congeners. Zootaxa 4980(1): 1–27. https://doi.org/10.11646/zootaxa.4980.1.1

Agung AP, Chornelia A, Grismer LL, Grismer JL, Quah ESH, Lu J, Tomlinson KW, Hughes AC (2022) Description of two new species of *Hemiphyllodactylus* (Reptilia: Gekkonidae) from karst landscapes in Yunnan, China, highlights complex conservation needs. Zoological Research 43(5): 767–786. https://doi.org/10.24272/j.issn.2095-8137.2022.105

Eliades SJ, Phimmachak S, Sivongxay N, Siler CD, Stuart BL (2019) Two new species of Hemiphyllodactylus (Reptilia: Gekkonidae) from Laos. Zootaxa 4577(1): 131–147. https://doi.org/10.11646/zootaxa.4577.1.8

Grismer LL, Wood Jr PL, Anuar S, Muin MA, Quah ES, Mcguire JA, Brown RM, Ngo TV, Hong Thai P (2013) Integrative taxonomy uncovers high levels of cryptic species diversity in *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) and the description of a new species from Peninsular Malaysia. Zoological Journal of the Linnean Society 169(4): 849–880. https://doi.org/10.1111/zoj.12064

Grismer LL, Wood Jr PL, Zug GR, Thura MK, Zin T, Quah ESH, Murdoch ML, Grismer MS, Lin A, Kyaw H, Lwin N (2018) Twelve new species of *Cyrtodactylus* Gray (Squamata: Gekkonidae) from isolated limestone habitats in east–central and southern Myanmar demonstrate high localized diversity and unprecedented microendemism. Zoological Journal of the Linnean Society 182(4): 862–959. https://doi.org/10.1093/zoolinnean/zlx057

Grismer LL, Chit MT, Pawangkhanant P, Nazarov RA, Zaw T, Poyarkov NA (2020) The phylogeny of *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) with a description of a new species from the Mangin Range, Sagaing Region, northern Myanmar. Journal of Natural History 54(29–30): 1913–1931. https://doi.org/10.1080/00222933.2020.1833095

Guo WB, Zhou KY, Yan J, Li P (2015) A new species of *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) from western Yunnan, China. Zootaxa 3974(3): 377–390. https://doi.org/10.11646/zootaxa.3974.3.5

Huelsenbeck JP, Ronquist F, Nielsen R, Bollback JP (2001) Bayesian inference of phylogeny and its impact on evolutionary biology. Science 294(5550): 2310–2314. https://doi.org/10.1126/science.1065889

Kalyaanamoorthy S, Minh BQ, Wong TK, Von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14(6): 587–589. https://doi.org/10.1038/nmeth.4285

Luu VQ, Nguyen TH, Do QH, Pham CT, Hoang TT, Nguyen TQ, Le MD, Ziegler T, Grismer JL, Grismer LL (2023) A new species of *Hemiphyllodactylus* (Squamata, Gekkonidae) from Ha Giang Province, Vietnam. Zookeys 1167: 353–382. https://doi.org/10.3897/zookeys.1167.103713

Luu VQ, Hoang TT, Ha HB, Grismer JL, Murdoch M, Sitthivong S, Phimphasone V, Grismer LL (2024) Integrative taxonomy reveals two new species of karst-dwelling *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) from the border region of Laos and Vietnam. Zootaxa 5486(1): 71–108. https://doi.org/10.11646/zootaxa.5486.1.3

Macey JJ, Larson A, Ananjeva NB, Fang Z, Papenfuss TJ (1997) Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Molecular Biology and Evolution 14(1): 91–104. https://doi.org/10.1093/oxfordjournals.molbev.a025706

Minh BQ, Nguyen MA, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30(5): 1188–1195. https://doi.org/10.1093/molbev/mst024

R Core Team (2021) R: A Language and Environment for Statistical Computing; R Foundation for Statistical Computing: Vienna, Austria. https://www.R-project.org/ [accessed on 15 December 2024]

Tamura K, Stecher G, Kumar S (2021) MEGA11: Molecular evolutionary genetics analysis version 11. Molecular Biology and Evolution 38(7): 3022–3027. https://doi.org/10.1093/molbev/msab120

Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22(22): 4673–4680. https://doi.org/10.1093/nar/22.22.4673

Uetz P, Freed P, Aguilar R, Reyes F, Hošek J [Eds] (2024) The Reptile Database. http://www.reptile-database.org [Accessed 8 October 2024]

Wilcox TP, Zwickl DJ, Heath TA, Hillis DM (2002) Phylogenetic relationships of the Dwarf Boas and a comparison of Bayesian and bootstrap measures of phylogenetic support. Molecular Phylogenetics and Evolution 25(2): 361–371. https://doi.org/10.1016/S1055-7903(02)00244-0

Yushchenko PV, Grismer LL, Agin AM, Dac LX, Poyarkov NA (2023) A new species of the genus *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) from a lowland monsoon forest in Southern Vietnam. Zootaxa 5306(5): 537–550. https://doi.org/10.11646/zootaxa.5306.5.2

Zhou HX, Li SM, Shen ZQ, Liu S, Rao DQ (2024a) A new species of *Hemiphyllodactylus* (Squamata, Gekkonidae) from southwest Yunnan, China. Zookeys 1197: 197–213. https://doi.org/10.3897/zookeys.1197.117359

Zhou HX, Li XY, Yuan CY, Cui LW, Liu S, Rao DQ (2024b) Integrative taxonomy revealed high diversity of *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) and the description of three new species from Yunnan Province, China. Animals 14(20): 3030. https://doi.org/10.3390/ani14203030

Zug GR (2010) Speciation and dispersal in a low diversity taxon: The slender geckos *Hemiphyllodactylus* (Reptilia, Gekkonidae). Smithsonian Contributions to Zoology 631(631): 1–70. https://doi.org/10.5479/si.00810282.631

Supplementary material 1

Principal component analysis scores of *Hemiphyllodactylus laowozhenensis* sp. nov., *H. gengmaensis* and *H. changningensis* and *H. zhutangxiangensis* (clade 3)

Authors: Hongxin Zhou, Xiaohan Wang, Liangwei Cui1, Dongru Zhang, Ziqi Shen, Xiuyan Li, Shuo Liu, Dingqi Rao

Data type: xlsx

Explanation note: Abbreviations are listed in the Materials and methods.

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/zse.101.138964.suppl1

Supplementary material 2

Morphometric and meristic data used in the analyses from specimens of Hemiphyllodactylus members within clade 3

Authors: Hongxin Zhou, Xiaohan Wang, Liangwei Cui1, Dongru Zhang, Ziqi Shen, Xiuyan Li, Shuo Liu, Dingqi Rao

Data type: xlsx

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/zse.101.138964.suppl2